

GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - protein search, using sw model  
Run on: November 16, 2006, 22:47:18 ; Search time 156 Seconds  
(without alignments)  
35.578 Million cell updates/sec

Title: PRSSRQ  
Perfect score: 29  
Sequence: 1 fssrq 6

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Maximum Match 0%  
Maximum Match 0%  
Listing first 45 summaries

Database : UniProt\_7.2:  
1: uniprot\_sprot:  
2: uniprot\_trembl:  
\* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the total score distribution, and is derived by analysis of the total score distribution.

1: uniprot\_sprot:  
2: uniprot\_trembl:  
\*

SUMMARIES

Result No.	Score	Query	Match Length	DB ID	Description
1	29	100.0	99	2 Q5NN07_ZYMMO	Q5NN07 zyomonas m
2	29	100.0	296	2 Q8ZT49_PVRAE	Q8ZT49 pyrobaculum
3	29	100.0	487	2 Q5L502_CHLAB	Q5L502 chlamydophili
4	29	100.0	497	1 PEN3_ADE12	PEN3 human adeno
5	29	100.0	555	2 Q2KRX5_ADE16	Q2KRX5 human adeno
6	29	100.0	621	2 Q9UDG2_SCHPO	Q9UDG2 schizosacch
7	29	100.0	629	2 Q4FED3_CHLAB	Q4FED3 chlamydophili
8	29	100.0	648	2 Q4VA42_MOUSE	Q4VA42 mus musculus
9	29	100.0	648	2 Q8BHK4_MOUSE	Q8BHK4 m 13 days e
10	29	100.0	649	2 Q6P7P7_RAT	Q6P7P7 ratius norv
11	29	100.0	708	2 Q9L0G1_ARATH	Q9L0G1 arabidopsis
12	29	100.0	1033	1 YD56_SCHPO	Q10309 schizosacch
13	29	100.0	1172	2 Q5CLH4_CRYHO	Q5CLH4 cryptospori
14	29	100.0	1173	2 Q5CV20_CRYPV	Q5CV20 cryptospori
15	29	100.0	1889	2 Q4IIK4_GIBZE	Q4IIK4 gibberella

#### ALIGNMENTS

RESULT 1  
Q5NN07\_ZYMMO  
ID Q5NN07\_ZYMMO PRELIMINARY; PRT; 99 AA.  
AC Q5NN07; DT 01-FEB-2005; integrated into UniProtKB/TrEMBL.  
DE Hypothetical protein.  
GN OrderedLocusNames:ZM01629;  
OS Zymomonas mobilis.  
OC Bacteria; Proteobacteria; Alphaproteobacteria; Sphingomonadales;  
SP Sphingomonadaceae; Zymomonas.  
RN [1] NCBI\_TaxID:542;  
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
STRAIN=ATCC 3.821 / 2M4 / CP4;  
PMID:15523456; DOI:10.1038/nbt01045;  
RC BX  
RA Seo J.-S., Chong H., Park H.-S., Yoon K.-O., Jung C., Kim J.-J.,  
RA Hong J.-H., Kim J.-H., Kii J.-I., Park C.-J., Oh H.-M.,  
RA Lee J.-S., Jin S.-J., Um H.-W., Lee H.-J., Oh S.-J., Kim J.Y.,  
RA Kang H.-I., Lee S.-Y., Lee K.-J., Kang H.-S.;  
RA RT  
"The genome sequence of the ethanologenic bacterium *Zymomonas mobilis*

GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Biocceleration Ltd.

**OM protein - protein search, using sw model**  
Run on: November 16, 2006, 22:52:33 ; Search time 20.4 Seconds  
(without alignments)  
28.299 Million cell updates/sec

Title: PRSSRQ  
Perfect score: 29  
Sequence: 1 frsrrq 6

Scoring table: BLOSUM62  
gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

POST-processing: Minimum Match 0‡  
Maximum Match 0‡  
Listing first 45 summaries

Database : PIR:80:\*

1: Pir1:\*

2: Pir2:\*

3: Pir3:\*

4: Pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query	Match Length	DB ID	Description
1	29	100.0	497	1 S33938	penton protein (II) hypothetical protein probable calcium-t HTH transcription Hth transcription indole-3-glycerol- indole-3-glycerol- hypothetical protein angiotensin receptor penton protein (II) penton protein (II) GGDP family protein phototransducer, m
2	29	100.0	621	2 T39204	
3	29	100.0	1033	2 T39203	
4	26	89.7	143	2 B86624	
5	26	89.7	143	2 C72000	
6	26	89.7	248	1 S50179	
7	26	89.7	248	2 C40635	
8	26	89.7	266	2 AB2270	
9	26	89.7	380	2 I38435	
10	26	89.7	544	1 S41389	
11	26	89.7	571	1 XZADH5	
12	26	89.7	589	2 AG2932	
13	26	89.7	589	2 H98349	

RESULT 1  
S33938

penton protein (III) - human adenovirus 12  
C:Species: Mastadenovirus H12 (human adenovirus 12)  
C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 09-Jul-2004  
C:Accession: S33938  
R:Spengel, J.  
submitted to the EMBL Data Library, June 1993  
A:Reference number: S33938  
A:Accession: S33938  
A:Status: preliminary  
A: Molecule type: DNA  
A:Residues: 1-497 <SPR>  
A:Cross-references: UNIPROT:P36716; UNIPARC:UPI00013159C; EMBL:X73487;  
NTD:g113361; PID:CAA51987; PID:g313372  
C:Superfamily: adenovirus penton protein

#### ALIGNMENTS

Query Match 100.0%; Score 29; DB 1; Length 497;  
Best Local Similarity 100.0%; Prod. No. 18;  
Matches 6; Conservative 0; Mismatches 0; Gaps 0;

GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Biocceleration Ltd.

**OM protein - protein search, using sw model**

Run on: November 16, 2006, 22:46:28 ; Search time 117.6 Seconds  
(without alignments)

(23.37 Million cell updates/sec  
23.37 Million cell updates/sec

Title: PRSSRQ  
Perfect score: 29

Sequence: 1. fssrq 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0‡

Maximum Match 10‡

Listing first 45 summaries

Database : A\_Geneseq\_8:\*

1: geneseqp1980s:\*

2: geneseqp1990s:\*

3: geneseqp2000s:\*

4: geneseqp2001s:\*

5: geneseqp2002s:\*

6: geneseqp2003as:\*

7: geneseqp2003bs:\*

8: geneseqp2004s:\*

9: geneseqp2005s:\*

10: geneseqp2006s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the total score distribution, and is derived by analysis of the total score distribution.

**SUMMARIES**

Result No.	Score	Query	Match	Length	DB ID	Description
1	29	100.0	6	8	ADU05742	Adu05742 Kallikrein
2	29	100.0	6	9	ADZ79589	Adz79589 Wound hea
3	29	100.0	6	9	AEB97528	Aeb97528 Kallikrein
4	29	100.0	6	9	AEC12751	Aec12751 Substrate
5	29	100.0	168	8	ADY05168	Ady05168 Plant ful
6	29	100.0	984	7	ABMB8980	Abmb8980 Rice abio
7	29	100.0	1080	8	ADN19557	Adn19557 Bacterial

**ALIGNMENTS**

**RESULT 1**

ADU05742

27-JAN-2005 (first entry)

DT

Unidentified.

XX

AC

ADU05742;

ID

ADU05742 standard, peptide, 6 Å.

XX

DE

Kallikrein substrate Peptide #1.

XX

KW

antimicrobial; analgesic; anesthetic; vulnerary; kallikrein inhibitor;

XX

wound dressing; oligopeptidic sequence; kallikrein.

XX

OS

GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - protein search, using sw model  
Run on: November 16, 2006, 22:46:28 ; Search time 176.4 Seconds  
(without alignments)  
23.327 Million cell updates/sec

Title: M1SLMKRQP  
Perfect score: 44  
Sequence: 1 m1slmkrpq 9

Scoring table: BLOSUM62  
Gapop 10.0 Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_B:\*

1: geneseqp1980s:\*

2: geneseqp1990s:\*

3: geneseqp2000s:\*

4: geneseqp2001s:\*

5: geneseqp2002s:\*

6: geneseqp2003as:\*

7: geneseqp2003bs:\*

8: geneseqp2004s:\*

9: geneseqp2005s:\*

10: geneseqp2006s:\*

8 39 88.6 64 2 AAW77418 Kininogen  
9 39 88.6 268 8 ADP43683 Human PM  
10 39 88.6 268 8 ABM83721 Human dia  
11 39 88.6 304 6 ABP70801 Human ext  
12 39 88.6 304 8 ABM83720 Human dia  
13 39 88.6 322 6 ABP70799 Human ext  
14 39 88.6 326 8 ABM83717 Human dia  
15 39 88.6 329 6 ABU52044 Human pro  
16 39 88.6 329 8 ABM83716 Human dia  
17 39 88.6 357 6 ABR1202 Human DIT  
18 39 88.6 358 6 ABP70800 Human ext  
19 39 88.6 362 9 AEB32339 Human pro  
20 39 88.6 362 9 AEB32341 Human pro  
21 39 88.6 390 6 ABU99149 Novel hum  
22 39 88.6 390 8 ADM93863 Human NOV  
23 39 88.6 390 8 ADT04032 Human pro  
24 39 88.6 390 8 ADS33172 Novel hum  
25 39 88.6 392 8 ABM83719 Human dia  
26 39 88.6 398 6 ABU99143 Novel hum  
27 39 88.6 398 8 ADM93851 Human NOV  
28 39 88.6 398 8 ABM83718 Human dia  
29 39 88.6 398 8 ADS33160 Novel hum  
30 39 88.6 427 8 ADE76864 Human pro  
31 39 88.6 427 8 ABM83715 Human dia  
32 39 88.6 427 8 ABM80523 Tumour-as  
33 39 88.6 427 8 ADQ39518 Human myo  
34 39 88.6 427 8 ADQ39516 Human myo  
35 39 88.6 427 8 ADS33164 Novel hum  
36 39 88.6 579 9 AEB32342 Human pro  
37 39 88.6 579 9 AEB32338 Human pro  
38 39 88.6 612 8 ADS33142 Novel hum  
39 39 88.6 615 6 ABU99144 Novel hum  
40 39 88.6 615 8 ADM93853 Human NOV  
41 39 88.6 615 8 ADS33162 Novel hum  
42 39 88.6 616 8 ADS33154 Novel hum  
43 39 88.6 621 8 ADS33156 Novel hum  
44 39 88.6 621 8 ADS33184 Novel hum  
45 39 88.6 622 8 ADS33158 Novel hum  
7 39 88.6 OS Unidentified.

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### ALIGNMENTS

#### RESULT 1

ADU05743 standard; peptide: 9 AA.  
ID ADU05743

#### SUMMARIES

Result No.	Query	Match	Length	DB ID	Description
1	44 100.0	9 8	ADU05743		AdU05743 Kallikrein
2	44 100.0	9 9	ADZ79590		AdZ79590 Wound hea
3	44 100.0	9 9	ABB97529		Aeb97529 Kallikrein
4	44 100.0	9 9	AEC32752		Aec32752 Substrate
5	39 88.6	16 2	AAM54320		Aam54320 Bradykini
6	39 88.6	60 4	ABG21097		Abg21097 Novel hum
7	39 88.6	64 2	AAM54341		Aam54341 Bradykini